

SEQUENCE LISTING

(1) GENERAL INFORMATION

- (i) APPLICANT: Falb, Dean
- (ii) TITLE OF THE INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF
CARDIOVASCULAR DISEASE
- (iii) NUMBER OF SEQUENCES: 44
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: PENNIE & EDMONDS LLP
 - (B) STREET: 1155 Avenue of the Americas
 - (C) CITY: New York
 - (D) STATE: NY
 - (E) COUNTRY: USA
 - (F) ZIP: 10036-2711
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Diskette
 - (B) COMPUTER: IBM Compatible
 - (C) OPERATING SYSTEM: DOS
 - (D) SOFTWARE: FastSEQ Version 2.0
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: 08/799,910
 - (B) FILING DATE: 13-FEB-1997
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: 60/011,787
 - (B) FILING DATE: 16-FEB-1996
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Coruzzi, Laura A
 - (B) REGISTRATION NUMBER: 30,742
 - (C) REFERENCE/DOCKET NUMBER: 7853-067-999
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (212)7909090
 - (B) TELEFAX: (212)8699741
 - (C) TELEX: 66141 PENNIE

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1953 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: Coding Sequence
 - (B) LOCATION: 162...1871
 - (D) OTHER INFORMATION:
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACCAGATC	GGAGCCGGGC	GGAGGGGAGG	GGGGAAAGAG	GAGCGCAGGG	TGAGAGTGAG	60
CCGCAGGCTT	CGGGAGGCCA	GGGGGCGGGG	GGAGCAGCGC	CGAGGYCGCC	GCCTCCGCCT	120
CCGCCGCCTA	GGACTAGGGG	GTGGGGGACG	GACAAGCCCC	G ATG CCG GGG GAG ACG		176
				Met Pro Gly Glu Thr		
				1	5	
GAA GAG CCG AGA CCC CCG GAG CAG CAG GAC CAG GAA GGG GGA GAG GCG						224
Glu Glu Pro Arg Pro Pro Glu Gln Gln Asp Gln Glu Gly Gly Glu Ala						
	10			15	20	
GCC AAG GCG GCT CCG GAG GAG CCC CAA CAA CGG CCC CCT GAG GCG GTC						272
Ala Lys Ala Ala Pro Glu Glu Pro Gln Gln Arg Pro Pro Glu Ala Val						
	25			30	35	
GCG GCG GCG CCT GCA GGG ACC ACT AGC AGC CGC GTG CTG AGG GGA GGT						320
Ala Ala Ala Pro Ala Gly Thr Thr Ser Ser Arg Val Leu Arg Gly Gly						
	40			45	50	
CGG GAC CGA GGC CGG GCC GCT GCG GCC GCC GCC GCA GCT GTG TCC						368
Arg Asp Arg Gly Arg Ala Ala Ala Ala Ala Ala Ala Val Ser						
	55			60	65	
CGC CGG AGG AAG GCC GAG TAT CCC CGC CGG CGG AGG AGC AGC CCC AGC						416
Arg Arg Arg Lys Ala Glu Tyr Pro Arg Arg Arg Arg Ser Ser Pro Ser						
	70			75	80	85
GCC AGG CCT CCC GAC GTC CCC GGG CAG CAG CCC CAG GCC GCG AAG TCC						464
Ala Arg Pro Pro Asp Val Pro Gly Gln Gln Pro Gln Ala Ala Lys Ser						
	90			95	100	
CCG TCT CCA GTT CAG GGC AAG AAG AGT CCG CGA CTC CTA TGC ATA GAA						512
Pro Ser Pro Val Gln Gly Lys Lys Ser Pro Arg Leu Leu Cys Ile Glu						
	105			110	115	
AAA GTA ACA ACT GAT AAA GAT CCC AAG GAA GAA AAA GAG GAA GAA GAC						560
Lys Val Thr Thr Asp Lys Asp Pro Lys Glu Glu Lys Glu Glu Glu Asp						
	120			125	130	
GAT TCT GCC CTC CCT CAG GAA GTT TCC ATT GCT GCA TCT AGA CCT AGC						608
Asp Ser Ala Leu Pro Gln Glu Val Ser Ile Ala Ala Ser Arg Pro Ser						
	135			140	145	
CGG GGC TGG CGT AGT AGT AGG ACA TCT GTT TCT CGC CAT CGT GAT ACA						656
Arg Gly Trp Arg Ser Ser Arg Thr Ser Val Ser Arg His Arg Asp Thr						
	150			155	160	165
GAG AAC ACC CGA AGC TCT CGG TCC AAG ACC GGT TCA TTG CAG CTC ATT						704
Glu Asn Thr Arg Ser Ser Arg Ser Lys Thr Gly Ser Leu Gln Leu Ile						
	170			175	180	
TGC AAG TCA GAA CCA AAT ACA GAC CAA CTT GAT TAT GAT GTT GGA GAA						752
Cys Lys Ser Glu Pro Asn Thr Asp Gln Leu Asp Tyr Asp Val Gly Glu						
	185			190	195	
GAG CAT CAG TCT CCA GGT GGC ATT AGT GGT GAA GAG GAA GAG GAG GAG						800
Glu His Gln Ser Pro Gly Gly Ile Ser Gly Glu Glu Glu Glu Glu Glu						
	200			205	210	
GAA GAA GAG ATG TTA ATC AGT GAA GAG GAG ATA CCA TTC AAA GAT GAT						848
Glu Glu Glu Met Leu Ile Ser Glu Glu Glu Ile Pro Phe Lys Asp Asp						
	215			220	225	
CCA AGA GAT GAG ACC TAC AAA CCC CAC TTA GAA AGG GAA ACC CCA AAG						896
Pro Arg Asp Glu Thr Tyr Lys Pro His Leu Glu Arg Glu Thr Pro Lys						
	230			235	240	245
CCA CGG AGA AAA TCA GGG AAG GTA AAA GAA GAG AAG GAG AAG AAG GAA						944

Pro	Arg	Arg	Lys	Ser 250	Gly	Lys	Val	Lys	Glu 255	Glu	Lys	Glu	Lys	Lys 260	Glu		
ATT	AAA	GTG	GAA	GTA	GAG	GTG	GAG	GTG	AAA	GAA	GAG	GAG	AAT	GAA	ATT	992	
Ile	Lys	Val	Glu 265	Val	Glu	Val	Glu	Val	Lys 270	Glu	Glu	Glu	Asn 275	Glu	Ile		
AGA	GAG	GAT	GAG	GAA	CCT	CCA	AGG	AAG	AGA	GGA	AGA	AGA	CGA	AAA	GAT	1040	
Arg	Glu	Asp 280	Glu	Glu	Pro	Pro	Arg 285	Lys	Arg	Gly	Arg	Arg 290	Arg	Lys	Asp		
GAC	AAA	AGT	CCA	CGT	TTA	CCC	AAA	AGG	AGA	AAA	AAG	CCT	CCA	ATC	CAG	1088	
Asp	Lys 295	Ser	Pro	Arg	Leu	Pro 300	Lys	Arg	Arg	Lys	Lys 305	Pro	Pro	Ile	Gln		
TAT	GTC	CGT	TGT	GAG	ATG	GAA	GGA	TGT	GGA	ACT	GTC	CTT	GCC	CAT	CCT	1136	
Tyr	Val	Arg	Cys	Glu	Met 315	Glu	Gly	Cys	Gly	Thr 320	Val	Leu	Ala	His	Pro 325		
CGC	TAT	TTG	CAG	CAC	CAC	ATT	AAA	TAC	CAG	CAT	TTG	CTG	AAG	AAG	AAA	1184	
Arg	Tyr	Leu	Gln	His 330	His	Ile	Lys	Tyr	Gln 335	His	Leu	Leu	Lys	Lys 340	Lys		
TAT	GTA	TGT	CCC	CAT	CCC	TCC	TGT	GGA	CGA	CTC	TTC	AGG	CTT	CAG	AAG	1232	
Tyr	Val	Cys	Pro 345	His	Pro	Ser	Cys	Gly 350	Arg	Leu	Phe	Arg	Leu 355	Gln	Lys		
CAA	CTT	CTG	CGA	CAT	GCC	AAA	CAT	CAT	ACA	GAT	CAA	AGG	GAT	TAT	ATC	1280	
Gln	Leu	Leu 360	Arg	His	Ala	Lys	His 365	His	Thr	Asp	Gln	Arg 370	Asp	Tyr	Ile		
TGT	GAA	TAT	TGT	GCT	CGG	GCC	TTC	AAG	AGT	TCC	CAC	AAT	CTG	GCA	GTG	1328	
Cys	Glu 375	Tyr	Cys	Ala	Arg	Ala 380	Phe	Lys	Ser	Ser	His 385	Asn	Leu	Ala	Val		
CAC	CGG	ATG	ATT	CAC	ACT	GGC	GAG	AAG	CCA	TTA	CAA	TGT	GAG	ATC	TGT	1376	
His	Arg	Met	Ile	His	Thr 395	Gly	Glu	Lys	Pro	Leu 400	Gln	Cys	Glu	Ile	Cys 405		
GGA	TTT	ACT	TGT	CGA	CAA	AAG	GCA	TCT	CTT	AAT	TGG	CAC	ATG	AAG	AAA	1424	
Gly	Phe	Thr	Cys	Arg 410	Gln	Lys	Ala	Ser	Leu 415	Asn	Trp	His	Met	Lys 420	Lys		
CAT	GAT	GCA	GAC	TCC	TTC	TAC	CAG	TTT	TCT	TGC	AAT	ATC	TGT	GGC	AAA	1472	
His	Asp	Ala	Asp 425	Ser	Phe	Tyr	Gln	Phe 430	Ser	Cys	Asn	Ile	Cys 435	Gly	Lys		
AAA	TTT	GAG	AAG	AAG	GAC	AGC	GTA	GTG	GCA	CAC	AAG	GCA	AAA	AGC	CAC	1520	
Lys	Phe	Glu	Lys	Lys	Asp	Ser	Val 445	Val	Ala	His	Lys	Ala 450	Lys	Ser	His		
CCT	GAG	GTG	CTG	ATT	GCA	GAA	GCT	CTG	GCT	GCC	AAT	GCA	GGC	GCC	CTC	1568	
Pro	Glu 455	Val	Leu	Ile	Ala	Glu 460	Ala	Leu	Ala	Ala	Asn 465	Ala	Gly	Ala	Leu		
ATC	ACC	AGC	ACA	GAT	ATC	TTG	GGC	ACT	AAC	CCA	GAG	TCC	CTG	ACG	CAG	1616	
Ile	Thr	Ser	Thr	Asp 475	Ile	Leu	Gly	Thr	Asn 480	Pro	Glu	Ser	Leu	Thr 485	Gln		
CCT	TCA	GAT	GGT	CAG	GGT	CTT	CCT	CTT	CTT	CCT	GAG	CCC	TTG	GGA	AAC	1664	
Pro	Ser	Asp	Gly 490	Gln	Gly	Leu	Pro	Leu 495	Pro	Glu	Pro	Leu	Gly 500	Asn			
TCA	ACC	TCT	GGA	GAG	TGC	CTA	CTG	TTA	GAA	GCT	GAA	GGG	ATG	TCA	AAG	1712	
Ser	Thr	Ser	Gly 505	Glu	Cys	Leu	Leu 510	Leu	Glu	Ala	Glu	Gly 515	Met	Ser	Lys		

TCA	TAC	TGC	AGT	GGG	ACG	GAA	CGG	GTG	AGC	CTG	ATG	GCT	GAT	GGG	AAG	1760
Ser	Tyr	Cys	Ser	Gly	Thr	Glu	Arg	Val	Ser	Leu	Met	Ala	Asp	Gly	Lys	
		520					525					530				
ATC	TTT	GTG	GGA	AGC	GGC	AGC	AGT	GGA	GGC	ACT	GAA	GGG	CTG	GTT	ATG	1808
Ile	Phe	Val	Gly	Ser	Gly	Ser	Ser	Gly	Gly	Thr	Glu	Gly	Leu	Val	Met	
	535					540					545					
AAC	TCA	GAT	ATA	CTC	GGT	GCT	ACC	ACA	GAG	GTT	CTG	ATT	GAA	GAT	TCA	1856
Asn	Ser	Asp	Ile	Leu	Gly	Ala	Thr	Thr	Glu	Val	Leu	Ile	Glu	Asp	Ser	
550					555				560						565	
GAC	TCT	GCC	GGA	CCT	TAGTGGACAG	GAAGACTTGG	GGCATGGGAC	AGCTCAGACT	T							1912
Asp	Ser	Ala	Gly	Pro												
				570												
TGTATTTAAA	AGTTAAAAAG	GACAAAAAAA	AAAAAAAAAA	A												1953

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 570 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: unknown
 - (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein
- (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Pro	Gly	Glu	Thr	Glu	Glu	Pro	Arg	Pro	Pro	Glu	Gln	Gln	Asp	Gln	
1				5					10					15		
Glu	Gly	Gly	Glu	Ala	Ala	Lys	Ala	Ala	Pro	Glu	Glu	Pro	Gln	Gln	Arg	
			20					25					30			
Pro	Pro	Glu	Ala	Val	Ala	Ala	Ala	Pro	Ala	Gly	Thr	Thr	Ser	Ser	Arg	
			35				40					45				
Val	Leu	Arg	Gly	Gly	Arg	Asp	Arg	Gly	Arg	Ala	Ala	Ala	Ala	Ala	Ala	
	50					55				60						
Ala	Ala	Ala	Val	Ser	Arg	Arg	Arg	Lys	Ala	Glu	Tyr	Pro	Arg	Arg	Arg	
65					70				75					80		
Arg	Ser	Ser	Pro	Ser	Ala	Arg	Pro	Pro	Asp	Val	Pro	Gly	Gln	Gln	Pro	
				85				90					95			
Gln	Ala	Ala	Lys	Ser	Pro	Ser	Pro	Val	Gln	Gly	Lys	Lys	Ser	Pro	Arg	
			100					105					110			
Leu	Leu	Cys	Ile	Glu	Lys	Val	Thr	Thr	Asp	Lys	Asp	Pro	Lys	Glu	Glu	
		115					120					125				
Lys	Glu	Glu	Glu	Asp	Asp	Ser	Ala	Leu	Pro	Gln	Glu	Val	Ser	Ile	Ala	
	130					135					140					
Ala	Ser	Arg	Pro	Ser	Arg	Gly	Trp	Arg	Ser	Ser	Arg	Thr	Ser	Val	Ser	
145					150				155						160	
Arg	His	Arg	Asp	Thr	Glu	Asn	Thr	Arg	Ser	Ser	Arg	Ser	Lys	Thr	Gly	
				165				170						175		
Ser	Leu	Gln	Leu	Ile	Cys	Lys	Ser	Glu	Pro	Asn	Thr	Asp	Gln	Leu	Asp	
			180					185					190			
Tyr	Asp	Val	Gly	Glu	Glu	His	Gln	Ser	Pro	Gly	Gly	Ile	Ser	Gly	Glu	
	195						200					205				
Glu	Glu	Glu	Glu	Glu	Glu	Glu	Glu	Met	Leu	Ile	Ser	Glu	Glu	Glu	Ile	
	210					215					220					
Pro	Phe	Lys	Asp	Asp	Pro	Arg	Asp	Glu	Thr	Tyr	Lys	Pro	His	Leu	Glu	
225					230				235						240	
Arg	Glu	Thr	Pro	Lys	Pro	Arg	Arg	Lys	Ser	Gly	Lys	Val	Lys	Glu	Glu	
				245				250						255		
Lys	Glu	Lys	Lys	Glu	Ile	Lys	Val	Glu	Val	Glu	Val	Glu	Val	Lys	Glu	
		260					265					270				
Glu	Glu	Asn	Glu	Ile	Arg	Glu	Asp	Glu	Glu	Pro	Pro	Arg	Lys	Arg	Gly	
		275					280					285				

Arg	Arg	Arg	Lys	Asp	Asp	Lys	Ser	Pro	Arg	Leu	Pro	Lys	Arg	Arg	Lys
290						295					300				
Lys	Pro	Pro	Ile	Gln	Tyr	Val	Arg	Cys	Glu	Met	Glu	Gly	Cys	Gly	Thr
305					310					315					320
Val	Leu	Ala	His	Pro	Arg	Tyr	Leu	Gln	His	His	Ile	Lys	Tyr	Gln	His
				325					330					335	
Leu	Leu	Lys	Lys	Lys	Tyr	Val	Cys	Pro	His	Pro	Ser	Cys	Gly	Arg	Leu
			340					345					350		
Phe	Arg	Leu	Gln	Lys	Gln	Leu	Leu	Arg	His	Ala	Lys	His	His	Thr	Asp
		355					360					365			
Gln	Arg	Asp	Tyr	Ile	Cys	Glu	Tyr	Cys	Ala	Arg	Ala	Phe	Lys	Ser	Ser
	370					375					380				
His	Asn	Leu	Ala	Val	His	Arg	Met	Ile	His	Thr	Gly	Glu	Lys	Pro	Leu
385					390					395					400
Gln	Cys	Glu	Ile	Cys	Gly	Phe	Thr	Cys	Arg	Gln	Lys	Ala	Ser	Leu	Asn
				405					410					415	
Trp	His	Met	Lys	Lys	His	Asp	Ala	Asp	Ser	Phe	Tyr	Gln	Phe	Ser	Cys
			420					425					430		
Asn	Ile	Cys	Gly	Lys	Lys	Phe	Glu	Lys	Lys	Asp	Ser	Val	Val	Ala	His
		435					440					445			
Lys	Ala	Lys	Ser	His	Pro	Glu	Val	Leu	Ile	Ala	Glu	Ala	Leu	Ala	Ala
	450					455					460				
Asn	Ala	Gly	Ala	Leu	Ile	Thr	Ser	Thr	Asp	Ile	Leu	Gly	Thr	Asn	Pro
465					470					475					480
Glu	Ser	Leu	Thr	Gln	Pro	Ser	Asp	Gly	Gln	Gly	Leu	Pro	Leu	Leu	Pro
				485					490					495	
Glu	Pro	Leu	Gly	Asn	Ser	Thr	Ser	Gly	Glu	Cys	Leu	Leu	Leu	Glu	Ala
			500					505					510		
Glu	Gly	Met	Ser	Lys	Ser	Tyr	Cys	Ser	Gly	Thr	Glu	Arg	Val	Ser	Leu
		515					520					525			
Met	Ala	Asp	Gly	Lys	Ile	Phe	Val	Gly	Ser	Gly	Ser	Ser	Gly	Gly	Thr
	530					535					540				
Glu	Gly	Leu	Val	Met	Asn	Ser	Asp	Ile	Leu	Gly	Ala	Thr	Thr	Glu	Val
545					550					555					560
Leu	Ile	Glu	Asp	Ser	Asp	Ser	Ala	Gly	Pro						
				565					570						

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3103 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 288...1565
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GCACGAGCGG	AGAGCCGCGC	AGGGCGCGGG	CCGCGCGGGG	TGGGGCAGCC	GGAGCGCAGG	60
CCCCCGATCC	CCGGCGGGCG	CCCCCGGGCC	CCCGCGCGCG	CCCCGGCCTC	CGGGAGACTG	120
GCGCATGCCA	CGGAGCGCCC	CTCGGGCCGC	CGCCGCTCCT	GCCCGGGCCC	CTGCTGCTGC	180
TGCTGTCGCC	TGCGCCTGCT	GCCCCAACTC	GGCGCCCGAC	TCACAAAGAA	ACATCATGTT	240
CGTCTCTTAG	CAGGCAAACG	ACTTTTCTCC	TCGCCTCCTC	GCCCCGC	ATG TTC AGG	296
				Met	Phe Arg	
				1		
ACC AAA CGA	TCT GCG CTC	GTC CGG CGT	CTC TGG AGG	AGC CGT GCG	CCC	344
Thr Lys Arg	Ser Ala Leu	Val Arg Arg	Leu Trp	Arg Ser Arg	Ala Pro	
5		10		15		

GGC Gly 20	GGC Gly	GAG Glu	GAC Asp	GAG Glu 25	GAG Glu	GAG Glu	GGC Gly	GCA Ala	GGG Gly 30	GGA Gly	GGT Gly	GGA Gly	GGA Gly	GGA Gly	GGC Gly 35	392
GAG Glu	CTG Leu	CGG Arg	GGA Gly 40	GAA Glu	GGG Gly	GCG Ala	ACG Thr	GAC Asp 45	AGC Ser	CGA Arg	GCG Ala	CAT His	GGG Gly	GCC Ala 50	GGT Gly	440
GGC Gly	GGC Gly	GGC Gly	CCG Pro 55	GGC Gly	AGG Arg	GCT Ala	GGA Gly	TGC Cys 60	TGC Cys	CTG Leu	GGC Gly	AAG Lys	GCG Ala 65	GTG Val	CGA Arg	488
GGT Gly	GCC Ala	AAA Lys 70	GGT Gly	CAC His	CAC His	CAT His	CCC Pro 75	CAC His	CCG Pro	CCA Pro	GCC Ala	GCG Ala 80	GGC Gly	GCC Ala	GGC Gly	536
GCG Ala 85	GCC Ala	GGG Gly	GGC Gly	GCC Ala	GAG Glu	GCG Ala 90	GAT Asp	CTG Leu	AAG Lys	GCG Ala	CTC Leu 95	ACG Thr	CAC His	TCG Ser	GTG Val	584
CTC Leu 100	AAG Lys	AAA Lys	CTG Leu	AAG Lys	GAG Glu 105	CGG Arg	CAG Gln	CTG Leu	GAG Glu	CTG Leu 110	CTG Leu	CTC Leu	CAG Gln	GCC Ala	GTG Val 115	632
GAG Glu	TCC Ser	CGC Arg	GGC Gly 120	GGG Gly	ACG Thr	CGC Arg	ACC Thr	GCG Ala	TGC Cys 125	CTC Leu	CTG Leu	CTG Leu	CCC Pro	GGC Gly 130	CGC Arg	680
CTG Leu	GAC Asp	TGC Cys	AGG Arg 135	CTG Leu	GGC Gly	CCG Pro	GGG Gly	GCG Ala 140	CCC Pro	GCC Ala	GGC Gly	GCG Ala	CAG Gln 145	CCT Pro	GCG Ala	728
CAG Gln	CCG Pro	CCC Pro 150	TCG Ser	TCC Ser	TAC Tyr	TCG Ser	CTC Leu 155	CCC Pro	CTC Leu	CTG Leu	TGC Leu 160	AAA Cys	GTG Lys	TTC Val	Phe	776
AGG Arg 165	TGG Trp	CCG Pro	GAT Asp	CTC Leu	AGG Arg	CAT His 170	TCC Ser	TCG Ser	GAA Glu	GTC Val	AAG Lys 175	AGG Arg	CTG Leu	TGT Cys	TGC Cys	824
TGT Cys 180	GAA Glu	TCT Ser	TAC Tyr	GGG Gly	AAG Lys 185	ATC Ile	AAC Asn	CCC Pro	GAG Glu	CTG Leu 190	GTG Val	TGC Cys	TGC Cys	AAC Asn	CCC Pro 195	872
CAT His	CAC His	CTT Leu	AGC Ser	CGA Arg 200	CTC Leu	TGC Cys	GAA Glu	CTA Leu	GAG Glu 205	TCT Ser	CCC Pro	CCC Pro	CCT Pro 210	CCT Pro	TAC Tyr	920
TCC Ser	AGA Arg	TAC Tyr	CCG Pro 215	ATG Met	GAT Asp	TTT Phe	CTC Leu	AAA Lys 220	CCA Pro	ACT Thr	GCA Ala	GAC Asp	TGT Cys 225	CCA Pro	GAT Asp	968
GCT Ala	GTG Val	CCT Pro 230	TCC Ser	TCC Ser	GCT Ala	GAA Glu	ACA Thr 235	GGG Gly	GGA Gly	ACG Thr	AAT Asn	TAT Tyr 240	CTG Leu	GCC Ala	CCT Pro	1016
GGG Gly 245	GGG Gly	CTT Leu	TCA Ser	GAT Asp	TCC Ser	CAA Gln 250	CTT Leu	CTT Leu	CTG Leu	GAG Glu	CCT Pro 255	GGG Gly	GAT Asp	CGG Arg	TCA Ser	1064
CAC His 260	TGG Trp	TGC Cys	GTG Val	GTG Val	GCA Ala 265	TAC Tyr	TGG Trp	GAG Glu	GAG Glu	AAG Lys 270	ACG Thr	AGA Arg	GTG Val	GGG Gly	AGG Arg 275	1112
CTC Leu	TAC Tyr	TGT Cys	GTC Val	CAG Gln 280	GAG Glu	CCC Pro	TCT Ser	CTG Leu	GAT Asp 285	ATC Ile	TTC Phe	TAT Tyr	GAT Asp	CTA Leu 290	CCT Pro	1160

CAG GGG AAT GGC TTT TGC CTC GGA CAG CTC AAT TCG GAC AAC AAG AGT	1208
Gln Gly Asn Gly Phe Cys Leu Gly Gln Leu Asn S r Asp Asn Lys Ser	
295 300 305	
CAG CTG GTG CAG AAG GTG CGG AGC AAA ATC GGC TGC GGC ATC CAG CTG	1256
Gln Leu Val Gln Lys Val Arg Ser Lys Ile Gly Cys Gly Ile Gln Leu	
310 315 320	
ACG CGG GAG GTG GAT GGT GTG TGG GTG TAC AAC CGC AGC AGT TAC CCC	1304
Thr Arg Glu Val Asp Gly Val Trp Val Tyr Asn Arg Ser Ser Tyr Pro	
325 330 335	
ATC TTC ATC AAG TCC GCC ACA CTG GAC AAC CCG GAC TCC AGG ACG CTG	1352
Ile Phe Ile Lys Ser Ala Thr Leu Asp Asn Pro Asp Ser Arg Thr Leu	
340 345 350 355	
TTG GTA CAC AAG GTG TTC CCC GGT TTC TCC ATC AAG GCT TTC GAC TAC	1400
Leu Val His Lys Val Phe Pro Gly Phe Ser Ile Lys Ala Phe Asp Tyr	
360 365 370	
GAG AAG GCG TAC AGC CTG CAG CGG CCC AAT GAC CAC GAG TTT ATG CAG	1448
Glu Lys Ala Tyr Ser Leu Gln Arg Pro Asn Asp His Glu Phe Met Gln	
375 380 385	
CAG CCG TGG ACG GGC TTT ACC GTG CAG ATC AGC TTT GTG AAG GGC TGG	1496
Gln Pro Trp Thr Gly Phe Thr Val Gln Ile Ser Phe Val Lys Gly Trp	
390 395 400	
GGT CAG TGC TAC ACC CGC CAG TTC ATC AGC AGC TGC CCG TGC TGG CTA	1544
Gly Gln Cys Tyr Thr Arg Gln Phe Ile Ser Ser Cys Pro Cys Trp Leu	
405 410 415	
GAG GTC ATC TTC AAC AGC CGG TAGCCGCGTG CGGAGGGGAC AGAGCGTGAG CTGA	1599
Glu Val Ile Phe Asn Ser Arg	
420 425	
GCAGGCCACA CTTCAAACCTA CTTTGCTGCT AATATTTTCC TCCTGAGTGC TTGCTTTTCA	1659
TGCAAACCTCT TTGGTCGTTT TTTTGTGTTT TGTTGGTTGG TTTTCTTCTT CTCGTCCTCG	1719
TTTGTGTTCT GTTTTGTTTC GCTCTTTGAG AAATAGCTTA TGAAAAGAAT TGTTGGGGGT	1779
TTTTTTGGAA GAAGGGGCAG GTATGATCGG CAGGACACCC TGATAGGAAG AGGGGAAGCA	1839
GAAATCCAAG CACCACCAAA CACAGTGTAT GAAGGGGGGC GGTTCATCATT TCACTTGTC	1899
GGAGTGTGTG TGAGTGTGAG TGTGCGGCTG TGTGTGCACG CGTGTGCAGG AGCGGCAGAT	1959
GGGGAGACAA CGTGCTCTTT GTTTTGTGTC TCTTATGGAT GTCCCCAGCA GAGAGGTTTG	2019
CAGTCCCAAG CGGTGTCTCT CCTGCCCCCTT GGACACGCTC AGTGGGGCAG AGGCAGTACC	2079
TGGGCAAGCT GCGCGCTGGG GTCCCGAGCAG CTGCCAGGAG CACGGCTCTG TCCCCAGCCT	2139
GGGAAAGCCC CTGCCCCCTCC TCTCCCTCAT CAAGGACACG GGCCTGTCCA CAGGCTTCTG	2199
AGCAGCGAGC CTGCTAGTGG CCGAACCAGA ACCAATTATT TTCATCCTTG TCTTATTCCC	2259
TTCTTGCCAG CCCCTGCCAT TGTAGCGTCT TTCTTTTTTG GCCATCTGCT CCTGGATCTC	2319
CCTGAGATGG GCTTCCCAAG GGCTGCCGGG GCAGCCCCCT CACAGTATTG CTCACCCAGT	2379
GCCCTCTCCC CTCAGCCTCT CCCCTGCCTG CCCTGGTGAC ATCAGGTTTT TCCCGGACTT	2439
AGAAAACCAG CTCAGCACTG CCTGCTCCCA TCCTGTGTGT TAAGCTCTGC TATTAGGCCA	2499
GCAAGCGGGG ATGTCCCTGG GAGGGACATG CTTAGCAGTC CCCTTCCCTC CAAGAAGGAT	2559
TTGGTCCGTC ATAACCCAAG GTACCATCCT AGGCTGACAC CTAACCTCTC TTTCAATTCT	2619
TCTACAACCTC ATACACTCGT ATGATACTTC GACACTGTTC TTAGCTCAAT GAGCATGTTT	2679
AGACTTTAAC ATAAGCTATT TTTCTAACTA CAAAGGTTTA AATGAACAAG AGAAGCATTC	2739
TCATTGGAAA TTTAGCATTG TAGTGCTTTG AGAGAGAAAG GACTCCTGAA AAAAAACCTG	2799
AGATTTATTA AAGAAAAAAA TGTATTTTAT GTTATATATA AATATATTAT TACTTGTA	2859
TATAAAGACG TTTTATAAGC ATCATTATTT ATGTATTGTG CAATGTGTAT AAACAAGAAA	2919
AATAAAGAAA AGATGCACTT TGCTTTAATA TAAATGCAAA TAACAAATGC CAAATTA	2979
AAGATAAACA CAAGATTGGT GTTTTTTCTT ATGGGTGTTA TCACCTAGCT GAATGTTTTT	3039
CTAAAGGAGT TTATGTTCCA TTAAACGATT TTTAAATGT ACACTTGAAA AAAAAA	3099
AAAA	3103

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 426 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Phe	Arg	Thr	Lys	Arg	Ser	Ala	Leu	Val	Arg	Arg	Leu	Trp	Arg	Ser
1				5					10					15	
Arg	Ala	Pro	Gly	Gly	Glu	Asp	Glu	Glu	Glu	Gly	Ala	Gly	Gly	Gly	Gly
			20					25					30		
Gly	Gly	Gly	Glu	Leu	Arg	Gly	Glu	Gly	Ala	Thr	Asp	Ser	Arg	Ala	His
		35				40						45			
Gly	Ala	Gly	Gly	Gly	Gly	Pro	Gly	Arg	Ala	Gly	Cys	Cys	Leu	Gly	Lys
	50					55					60				
Ala	Val	Arg	Gly	Ala	Lys	Gly	His	His	His	Pro	His	Pro	Pro	Ala	Ala
65					70					75					80
Gly	Ala	Gly	Ala	Ala	Gly	Gly	Ala	Glu	Ala	Asp	Leu	Lys	Ala	Leu	Thr
				85					90					95	
His	Ser	Val	Leu	Lys	Lys	Leu	Lys	Glu	Arg	Gln	Leu	Glu	Leu	Leu	Leu
			100					105					110		
Gln	Ala	Val	Glu	Ser	Arg	Gly	Gly	Thr	Arg	Thr	Ala	Cys	Leu	Leu	Leu
		115				120						125			
Pro	Gly	Arg	Leu	Asp	Cys	Arg	Leu	Gly	Pro	Gly	Ala	Pro	Ala	Gly	Ala
	130					135					140				
Gln	Pro	Ala	Gln	Pro	Pro	Ser	Ser	Tyr	Ser	Leu	Pro	Leu	Leu	Leu	Cys
145					150					155					160
Lys	Val	Phe	Arg	Trp	Pro	Asp	Leu	Arg	His	Ser	Ser	Glu	Val	Lys	Arg
				165					170					175	
Leu	Cys	Cys	Cys	Glu	Ser	Tyr	Gly	Lys	Ile	Asn	Pro	Glu	Leu	Val	Cys
			180					185					190		
Cys	Asn	Pro	His	His	Leu	Ser	Arg	Leu	Cys	Glu	Leu	Glu	Ser	Pro	Pro
		195					200					205			
Pro	Pro	Tyr	Ser	Arg	Tyr	Pro	Met	Asp	Phe	Leu	Lys	Pro	Thr	Ala	Asp
	210					215					220				
Cys	Pro	Asp	Ala	Val	Pro	Ser	Ser	Ala	Glu	Thr	Gly	Gly	Thr	Asn	Tyr
225					230					235					240
Leu	Ala	Pro	Gly	Gly	Leu	Ser	Asp	Ser	Gln	Leu	Leu	Leu	Glu	Pro	Gly
				245					250					255	
Asp	Arg	Ser	His	Trp	Cys	Val	Val	Ala	Tyr	Trp	Glu	Glu	Lys	Thr	Arg
			260					265					270		
Val	Gly	Arg	Leu	Tyr	Cys	Val	Gln	Glu	Pro	Ser	Leu	Asp	Ile	Phe	Tyr
		275					280					285			
Asp	Leu	Pro	Gln	Gly	Asn	Gly	Phe	Cys	Leu	Gly	Gln	Leu	Asn	Ser	Asp
	290				295						300				
Asn	Lys	Ser	Gln	Leu	Val	Gln	Lys	Val	Arg	Ser	Lys	Ile	Gly	Cys	Gly
305					310					315					320
Ile	Gln	Leu	Thr	Arg	Glu	Val	Asp	Gly	Val	Trp	Val	Tyr	Asn	Arg	Ser
				325					330					335	
Ser	Tyr	Pro	Ile	Phe	Ile	Lys	Ser	Ala	Thr	Leu	Asp	Asn	Pro	Asp	Ser
		340						345					350		
Arg	Thr	Leu	Leu	Val	His	Lys	Val	Phe	Pro	Gly	Phe	Ser	Ile	Lys	Ala
		355					360					365			
Phe	Asp	Tyr	Glu	Lys	Ala	Tyr	Ser	Leu	Gln	Arg	Pro	Asn	Asp	His	Glu
	370					375					380				
Phe	Met	Gln	Gln	Pro	Trp	Thr	Gly	Phe	Thr	Val	Gln	Ile	Ser	Phe	Val
385					390					395					400
Lys	Gly	Trp	Gly	Gln	Cys	Tyr	Thr	Arg	Gln	Phe	Ile	Ser	Ser	Cys	Pro
				405					410					415	
Cys	Trp	Leu	Glu	Val	Ile	Phe	Asn	Ser	Arg						
			420					425							

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) NAME/KEY: Coding Sequence
(B) LOCATION: 90...938
(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCACGAGGT	TGCCCTGGCG	GAGCAGAGAC	AGGCCCTCGG	GGTGGAGGTC	TTTGTTTCA	60										
TAAGAGCCTG	AGAGAGATTT	TTCTAAGAT	ATG	TGT	AAC	ACA	CCA	ACG	TAC	TGT	113					
			Met	Cys	Asn	Thr	Pro	Thr	Tyr	Cys						
			1				5									
GAC	CTA	GGA	AAG	GCT	GCT	AAG	GAT	GTC	TTC	AAC	AAA	GGA	TAT	GGC	TTT	161
Asp	Leu	Gly	Lys	Ala	Ala	Lys	Asp	Val	Phe	Asn	Lys	Gly	Tyr	Gly	Phe	
	10					15					20					
GGC	ATG	GTC	AAG	ATA	GAC	CTG	AAA	ACC	AAG	TCT	TGT	AGT	GGA	GTG	GAA	209
Gly	Met	Val	Lys	Ile	Asp	Leu	Lys	Thr	Lys	Ser	Cys	Ser	Gly	Val	Glu	
25				30						35					40	
TTT	TCT	ACT	TCT	GGT	CAT	GCT	TAC	ACT	GAT	ACA	GGG	AAA	GCA	TCA	GGC	257
Phe	Ser	Thr	Ser	Gly	His	Ala	Tyr	Thr	Asp	Thr	Gly	Lys	Ala	Ser	Gly	
				45					50					55		
AAC	CTA	GAA	ACC	AAA	TAT	AAG	GTC	TGT	AAC	TAT	GGA	CTT	ACC	TTC	ACC	305
Asn	Leu	Glu	Thr	Lys	Tyr	Lys	Val	Cys	Asn	Tyr	Gly	Leu	Thr	Phe	Thr	
			60					65					70			
CAG	AAA	TGG	AAC	ACA	GAC	AAT	ACT	CTA	GGG	ACA	GAA	ATC	TCT	TGG	GAG	353
Gln	Lys	Trp	Asn	Thr	Asp	Asn	Thr	Leu	Gly	Thr	Glu	Ile	Ser	Trp	Glu	
		75					80					85				
AAT	AAG	TTG	GCT	GAA	GGG	TTG	AAA	CTG	ACT	CTT	GAT	ACC	ATA	TTT	GTA	401
Asn	Lys	Leu	Ala	Glu	Gly	Leu	Lys	Leu	Thr	Leu	Asp	Thr	Ile	Phe	Val	
	90					95					100					
CCG	AAC	ACA	GGA	AAG	AAG	AGT	GGG	AAA	TTG	AAG	GCC	TCC	TAT	AAA	CGG	449
Pro	Asn	Thr	Gly	Lys	Lys	Ser	Gly	Lys	Leu	Lys	Ala	Ser	Tyr	Lys	Arg	
105					110					115					120	
GAT	TGT	TTT	AGT	GTT	GGC	AGT	AAT	GTT	GAT	ATA	GAT	TTT	TCT	GGA	CCA	497
Asp	Cys	Phe	Ser	Val	Gly	Ser	Asn	Val	Asp	Ile	Asp	Phe	Ser	Gly	Pro	
				125					130					135		
ACC	ATC	TAT	GGC	TGG	GCT	GTG	TTG	GCC	TTC	GAA	GGG	TGG	CTT	GCT	GGC	545
Thr	Ile	Tyr	Gly	Trp	Ala	Val	Leu	Ala	Phe	Glu	Gly	Trp	Leu	Ala	Gly	
			140					145					150			
TAT	CAG	ATG	AGT	TTT	GAC	ACA	GCC	AAA	TCC	AAA	CTG	TCA	CAG	AAT	AAT	593
Tyr	Gln	Met	Ser	Phe	Asp	Thr	Ala	Lys	Ser	Lys	Leu	Ser	Gln	Asn	Asn	
		155					160					165				
TTC	GCC	CTG	GGT	TAC	AAG	GCT	GCG	GAC	TTC	CAG	CTG	CAC	ACA	CAT	GTG	641
Phe	Ala	Leu	Gly	Tyr	Lys	Ala	Ala	Asp	Phe	Gln	Leu	His	Thr	His	Val	
	170					175					180					
AAC	GAT	GGC	ACT	GAA	TTT	GGA	GGT	TCT	ATC	TAC	CAG	AAG	GTG	AAT	GAG	689
Asn	Asp	Gly	Thr	Glu	Phe	Gly	Gly	Ser	Ile	Tyr	Gln	Lys	Val	Asn	Glu	
185					190					195					200	

AAG ATT GAA ACA TCC ATA AAC CTT GCT TGG ACA GCT GGG AGT AAC AAC	737
Lys Ile Glu Thr Ser Ile Asn Leu Ala Trp Thr Ala Gly Ser Asn Asn	
205 210 215	
ACC CGT TTT GGC ATT GCT GCT AAG TAC ATG CTG GAT TGT AGA ACT TCT	785
Thr Arg Phe Gly Ile Ala Ala Lys Tyr Met Leu Asp Cys Arg Thr Ser	
220 225 230	
CTC TCT GCT AAA GTA AAT AAT GCC AGC CTG ATT GGA CTG GGT TAT ACT	833
Leu Ser Ala Lys Val Asn Asn Ala Ser Leu Ile Gly Leu Gly Tyr Thr	
235 240 245	
CAG ACC CTT CGA CCA GGA GTC AAA TTG ACT TTA TCA GCT TTA ATC GAT	881
Gln Thr Leu Arg Pro Gly Val Lys Leu Thr Leu Ser Ala Leu Ile Asp	
250 255 260	
GGG AAG AAC TTC AGT GCA GGA GGT CAC AAG GTT GGC TTG GGA TTT GAA	929
Gly Lys Asn Phe Ser Ala Gly Gly His Lys Val Gly Leu Gly Phe Glu	
265 270 275 280	
CTG GAA GCT TAATGTGGTT TGAGGAAAAGC ATCAGATTTG TCCCTGGAAG TGAAGAGAA	987
Leu Glu Ala	
ATGAACCCAC TATGTTTTGG CCTTAAAATT CTTCTGTGAA ATTTCAAAG TGTGAACTTT	1047
TTATTCTTCC AAAGAATTGT AATCCTCCCC ACACCTGAAGT CTAGGGGTTG CGAATCCCTC	1107
CTGAGGGAGA CGCTGAAGG CATGCCCTGGA AGTTGTTCATG TTTGTGCCAC GTTTCAGTTC	1167
AGTTCTGAAG TGTTATTAAA TGTGTTCCCTC AGCGACAGTG TAGCGTCATG TTAGAGGAGA	1227
CGATCTGACC CACCAGTTTG TACATCACGT CCTGCATGTC CCACACCATT TTTTCATGAC	1287
CTTGTAATAT ACTGGTCTCT GTGCTATAGT GGAATCTTTG GTTTTGCATC ATAGTAAAT	1347
AAAATAAACCATCATCATTT GGAACATAAA AAAAAAAAAA AAAAAA	1393

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 283 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Cys Asn Thr Pro Thr Tyr Cys Asp Leu Gly Lys Ala Ala Lys Asp	
1 5 10 15	
Val Phe Asn Lys Gly Tyr Gly Phe Gly Met Val Lys Ile Asp Leu Lys	
20 25 30	
Thr Lys Ser Cys Ser Gly Val Glu Phe Ser Thr Ser Gly His Ala Tyr	
35 40 45	
Thr Asp Thr Gly Lys Ala Ser Gly Asn Leu Glu Thr Lys Tyr Lys Val	
50 55 60	
Cys Asn Tyr Gly Leu Thr Phe Thr Gln Lys Trp Asn Thr Asp Asn Thr	
65 70 75 80	
Leu Gly Thr Glu Ile Ser Trp Glu Asn Lys Leu Ala Glu Gly Leu Lys	
85 90 95	
Leu Thr Leu Asp Thr Ile Phe Val Pro Asn Thr Gly Lys Lys Ser Gly	
100 105 110	
Lys Leu Lys Ala Ser Tyr Lys Arg Asp Cys Phe Ser Val Gly Ser Asn	
115 120 125	
Val Asp Ile Asp Phe Ser Gly Pro Thr Ile Tyr Gly Trp Ala Val Leu	
130 135 140	
Ala Phe Glu Gly Trp L u Ala Gly Tyr Gln Met Ser Phe Asp Thr Ala	
145 150 155 160	
Lys Ser Lys Leu Ser Gln Asn Asn Phe Ala Leu Gly Tyr Lys Ala Ala	
165 170 175	

Asp	Phe	Gln	Leu	His	Thr	His	Val	Asn	Asp	Gly	Thr	Glu	Phe	Gly	Gly
			180					185					190		
Ser	Ile	Tyr	Gln	Lys	Val	Asn	Glu	Lys	Ile	Glu	Thr	Ser	Ile	Asn	Leu
		195					200					205			
Ala	Trp	Thr	Ala	Gly	Ser	Asn	Asn	Thr	Arg	Phe	Gly	Ile	Ala	Ala	Lys
	210					215					220				
Tyr	Met	Leu	Asp	Cys	Arg	Thr	Ser	Leu	Ser	Ala	Lys	Val	Asn	Asn	Ala
	225				230					235					240
Ser	Leu	Ile	Gly	Leu	Gly	Tyr	Thr	Gln	Thr	Leu	Arg	Pro	Gly	Val	Lys
			245						250					255	
Leu	Thr	Leu	Ser	Ala	Leu	Ile	Asp	Gly	Lys	Asn	Phe	Ser	Ala	Gly	Gly
			260					265					270		
His	Lys	Val	Gly	Leu	Gly	Phe	Glu	Leu	Glu	Ala					
		275					280								

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1036 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 1...546
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ACG	AGC	CTA	GCC	CTG	GTG	CTC	AAC	CTG	CTG	CAG	ATC	CAG	AGG	AAT	GTC	48
Thr	Ser	Leu	Ala	Leu	Val	Leu	Asn	Leu	Leu	Gln	Ile	Gln	Arg	Asn	Val	
1				5					10					15		
ACT	CTC	TTC	CCC	GAG	GAG	GTG	ATC	GCC	ACC	ATC	TTT	TCC	TCC	GCC	TGG	96
Thr	Leu	Phe	Pro	Glu	Glu	Val	Ile	Ala	Thr	Ile	Phe	Ser	Ser	Ala	Trp	
			20					25					30			
TGG	GTC	CCT	CCC	TGC	TGC	GGG	ACA	GCA	GCT	GCT	GTT	GTT	GGC	CTA	CTG	144
Trp	Val	Pro	Pro	Cys	Cys	Gly	Thr	Ala	Ala	Ala	Val	Val	Gly	Leu	Leu	
		35				40						45				
TAC	CCC	TGT	ATC	GAC	AGT	CAC	CTC	GGA	GAA	CCC	CAC	AAA	TTT	AAG	AGA	192
Tyr	Pro	Cys	Ile	Asp	Ser	His	Leu	Gly	Glu	Pro	His	Lys	Phe	Lys	Arg	
	50					55					60					
GAA	TGG	GCC	AGT	GTC	ATG	CGC	TGC	ATA	GCA	GTT	TTT	GTT	GGC	ATT	AAC	240
Glu	Trp	Ala	Ser	Val	Met	Arg	Cys	Ile	Ala	Val	Phe	Val	Gly	Ile	Asn	
	65				70				75					80		
CAC	GCC	AGT	GCT	AAA	TTG	GAT	TTT	GCC	AAT	AAT	GTC	CAG	CTG	TCC	TTG	288
His	Ala	Ser	Ala	Lys	Leu	Asp	Phe	Ala	Asn	Asn	Val	Gln	Leu	Ser	Leu	
				85					90					95		
ACT	TTA	GCA	GCC	CTA	TCT	TTG	GGC	CTT	TGG	TGG	ACA	TTT	GAT	CGT	TCC	336
Thr	Leu	Ala	Ala	Leu	Ser	Leu	Gly	Leu	Trp	Trp	Thr	Phe	Asp	Arg	Ser	
			100					105					110			
AGA	AGT	GGC	CTT	GGG	CTG	GGG	ATC	ACC	ATA	GCT	TTT	CTA	GCT	ACG	CTG	384
Arg	Ser	Gly	Leu	Gly	Leu	Gly	Ile	Thr	Ile	Ala	Phe	Leu	Ala	Thr	Leu	
		115					120					125				
ATC	ACG	CAG	TTT	CTC	GTG	TAT	AAT	GGT	GTC	TAT	CAG	TAT	ACA	TCC	CCA	432
Ile	Thr	Gln	Phe	Leu	Val	Tyr	Asn	Gly	Val	Tyr	Gln	Tyr	Thr	Ser	Pro	

130	135	140	
GAT TTC CTC TAT ATT CGT TCT TGG CTC CCT TGT ATA TTT TTC TCA GGA			480
Asp Phe Leu Tyr Ile Arg Ser Trp Leu Pro Cys Ile Phe Phe Ser Gly			
145	150	155	160
GGC GTC ACG GTG GGG AAC ATA GGA CGA CAG TTA GCT ATG GGT GTT CCT			528
Gly Val Thr Val Gly Asn Ile Gly Arg Gln Leu Ala Met Gly Val Pro			
	165	170	175
GAA AAG CCC CAT AGT GAT TGAGTCTTCA AAACCACCGA TTCTGAGAGC AAGGAAGA			584
Glu Lys Pro His Ser Asp			
	180		
TTTTGGAAGA AAATCTGACT GTGGATTATG ACAAAGATTA TCTTTTTTCT TAAGTAATCT			644
ATTTAGATCG GGCTGACTGT ACAAATGACT CCTGGAAAAA ACTCTTCACC TAGTCTAGAA			704
TAGGGAGGTG GAGAATGATG ACTTACCCTG AAGTCTTCCC TTGACTGCCC GCACTGGCGC			764
CTGTCTGTGC CCTGGAGCAT TCTGCCCAGG CTACGTGGGT TCAGGCAGGT GGCAGCTTCC			824
CAAGTATTCG ATTTCAATCA TGTGATTAAA ACAAGTTGCC ATATTTCAAA AAAAAAAAAA			884
AAAAMCTCGA GACCAACCCG CAGTTTGTG TCAGTGCCCA AAGGAGGTAG GTTGATGGTG			944
CTTAACAAAC ATGAAGTATG GTGTAATAGG AATAATATTT ATCCNAAAGA TTTTAAAAA			1004
TAGGGCTGTG TTTAAAAA AAAAAAAAAA AA			1036

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 182 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Thr	Ser	Leu	Ala	Leu	Val	Leu	Asn	Leu	Leu	Gln	Ile	Gln	Arg	Asn	Val
1				5					10					15	
Thr	Leu	Phe	Pro	Glu	Glu	Val	Ile	Ala	Thr	Ile	Phe	Ser	Ser	Ala	Trp
			20					25					30		
Trp	Val	Pro	Pro	Cys	Cys	Gly	Thr	Ala	Ala	Ala	Val	Val	Gly	Leu	Leu
		35				40						45			
Tyr	Pro	Cys	Ile	Asp	Ser	His	Leu	Gly	Glu	Pro	His	Lys	Phe	Lys	Arg
	50					55					60				
Glu	Trp	Ala	Ser	Val	Met	Arg	Cys	Ile	Ala	Val	Phe	Val	Gly	Ile	Asn
65					70					75					80
His	Ala	Ser	Ala	Lys	Leu	Asp	Phe	Ala	Asn	Asn	Val	Gln	Leu	Ser	Leu
				85					90					95	
Thr	Leu	Ala	Ala	Leu	Ser	Leu	Gly	Leu	Trp	Trp	Thr	Phe	Asp	Arg	Ser
			100					105					110		
Arg	Ser	Gly	Leu	Gly	Leu	Gly	Ile	Thr	Ile	Ala	Phe	Leu	Ala	Thr	Leu
		115					120					125			
Ile	Thr	Gln	Phe	Leu	Val	Tyr	Asn	Gly	Val	Tyr	Gln	Tyr	Thr	Ser	Pro
	130					135					140				
Asp	Phe	Leu	Tyr	Ile	Arg	Ser	Trp	Leu	Pro	Cys	Ile	Phe	Phe	Ser	Gly
145					150					155					160
Gly	Val	Thr	Val	Gly	Asn	Ile	Gly	Arg	Gln	Leu	Ala	Met	Gly	Val	Pro
				165					170					175	
Glu	Lys	Pro	His	Ser	Asp										
				180											

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1228 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 1...468

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ATG TGT CAC TCT CGC AGC TGC CAC CCG ACC ATG ACC ATC CTG CAG GCC	48
Met Cys His Ser Arg Ser Cys His Pro Thr Met Thr Ile Leu Gln Ala	
1 5 10 15	
CCG ACC CCG GCC CCC TCC ACC ATC CCG GGA CCC CGG CGG GGC TCC GGT	96
Pro Thr Pro Ala Pro Ser Thr Ile Pro Gly Pro Arg Arg Gly Ser Gly	
20 25 30	
CCT GAG ATC TTC ACC TTC GAC CCT CTC CCG GAG CCC GCA GCG GCC CCT	144
Pro Glu Ile Phe Thr Phe Asp Pro Leu Pro Glu Pro Ala Ala Ala Pro	
35 40 45	
GCC GGG CGC CCC AGC GCC TCT CGC GGG CAC CGA AAG CGC AGC CGC AGG	192
Ala Gly Arg Pro Ser Ala Ser Arg Gly His Arg Lys Arg Ser Arg Arg	
50 55 60	
GTT CTC TAC CCT CGA GTG GTC CGG CGC CAG CTG CCA GTC GAG GAA CCG	240
Val Leu Tyr Pro Arg Val Val Arg Arg Gln Leu Pro Val Glu Glu Pro	
65 70 75 80	
AAC CCA GCC AAA AGG CTT CTC TTT CTG CTG CTC ACC ATC GTC TTC TGC	288
Asn Pro Ala Lys Arg Leu Leu Phe Leu Leu Thr Ile Val Phe Cys	
85 90 95	
CAG ATC CTG ATG GCT GAA GAG GGT GTG CCG GCG CCC CTG CCT CCA GAG	336
Gln Ile Leu Met Ala Glu Glu Gly Val Pro Ala Pro Leu Pro Pro Glu	
100 105 110	
GAC GCC CCT AAC GCC GCA TCC CTG GCG CCC ACC CCT GTG TCC CCC GTC	384
Asp Ala Pro Asn Ala Ala Ser Leu Ala Pro Thr Pro Val Ser Pro Val	
115 120 125	
CTC GAG CCC TTT AAT CTG ACT TCG GAG CCC TCG GAC TAC GCT CTG GAC	432
Leu Glu Pro Phe Asn Leu Thr Ser Glu Pro Ser Asp Tyr Ala Leu Asp	
130 135 140	
CTC AGC ACT TTC CTC CAG CAA CAC CCG GCC GCC TTC TAACTGTGAC TCCCCG	484
Leu Ser Thr Phe Leu Gln Gln His Pro Ala Ala Phe	
145 150 155	
CACTCCCCAA AAAGAATCCG AAAAACCACA AAGAAACACC AGGCGTACCT GGTGCGCGAG	544
AGCGTATCCC CAACTGGGAC TTCCGAGGCA ACTTGAAGTC AGAACACTAC AGCGGAGACG	604
CCACCCGGTG CTTGAGGCGG GACCGAGGCG CACAGAGACC GAGGCGCATA GAGACCGAGG	664
CACAGCCCAG CTGGGGCTAG GCCCGGTGGG AAGGAGAGCG TCGTTAATTT ATTTCTTATT	724
GCTCCTAATT AATATTTATA TGTATTTATG TACGTCCTCC TAGGTGATGG AGATGTGTAC	784
GTAATATTTA TTTTAACTTA TGCAAGGGTG TGAGATGTTT CCTCTGCTGT AAATGCAGGT	844
CTCTTGGTAT TTATTGAGCT TTGTGGGACT GGTGGAAGCA GGACACCTGG AACTGCGGCA	904
AAGTAGGAGA AGAAATGGGG AGGACTCGGG TGGGGGAGGA CGTCCCGGCT GGGATGAAGT	964
CTGGTGGTGG GTCGTAAGTT TAGGAGGTGA CTGCATCCTC CAGCATCTCA ACTCCGTCTG	1024
TCTACTGTGT GAGACTTCGG CGGACCATTA GGAATGAGAT CCGTGAGATC CTTCCATCTT	1084
CTTGAAGTCG CCTTTAGGGT GGCTGCGAGG TAGAGGGTTG GGGGTTGGTG GGCTGTCACG	1144
GAGCGACTGT CGAGATCGCC TAGTATGTTT TGTGAACACA AATAAAATTG ATTTACTGTC	1204
AAAAAAAAAA AAAAAAACT CGAG	1228

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 156 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: unknown
 (D) TOPOLOGY: unknown

- (ii) MOLECULE TYPE: protein
 (v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Cys	His	Ser	Arg	Ser	Cys	His	Pro	Thr	Met	Thr	Ile	Leu	Gln	Ala
1				5					10					15	
Pro	Thr	Pro	Ala	Pro	Ser	Thr	Ile	Pro	Gly	Pro	Arg	Arg	Gly	Ser	Gly
		20						25					30		
Pro	Glu	Ile	Phe	Thr	Phe	Asp	Pro	Leu	Pro	Glu	Pro	Ala	Ala	Ala	Pro
		35					40					45			
Ala	Gly	Arg	Pro	Ser	Ala	Ser	Arg	Gly	His	Arg	Lys	Arg	Ser	Arg	Arg
	50					55					60				
Val	Leu	Tyr	Pro	Arg	Val	Val	Arg	Arg	Gln	Leu	Pro	Val	Glu	Glu	Pro
65					70					75				80	
Asn	Pro	Ala	Lys	Arg	Leu	Leu	Phe	Leu	Leu	Leu	Thr	Ile	Val	Phe	Cys
			85						90					95	
Gln	Ile	Leu	Met	Ala	Glu	Glu	Gly	Val	Pro	Ala	Pro	Leu	Pro	Pro	Glu
		100						105					110		
Asp	Ala	Pro	Asn	Ala	Ala	Ser	Leu	Ala	Pro	Thr	Pro	Val	Ser	Pro	Val
		115					120					125			
Leu	Glu	Pro	Phe	Asn	Leu	Thr	Ser	Glu	Pro	Ser	Asp	Tyr	Ala	Leu	Asp
	130					135					140				
Leu	Ser	Thr	Phe	Leu	Gln	Gln	His	Pro	Ala	Ala	Phe				
145					150						155				

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 3084 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: both
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA
 (ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
 (B) LOCATION: 1032...1736
 (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GAATTCGGCA	CGAGGMCAGG	AGCTCCTTTW	CTGCGTCTCC	CATCATGGGG	CTTAGGGTTG	60
AGTCTTCAGG	TTCTGGGGGC	AGGAAGGACG	GGCACTCAGG	AGGCCCCCTC	CCCATCCACA	120
GCCCCCTCTT	GGGAGGGGGG	AAACTTGGCA	ACCCGGGAGG	CATGTGGATC	TTTTCCTAAG	180
CAAGATGCTG	AGCTGGAAAG	ATGGGGGTGT	AAGGTAATGT	CCCAAAGTGA	AACTTTGCCA	240
GGCACTGGGA	GAGGCTGTGA	ACTCTTTTCT	GGCTTTAGAA	TTTAGGTCTA	GATCCCAAAA	300
GGCTAAGTAC	CCCCTGGGGG	CTAACCAGAG	GCATGCCTGG	GCTGAGCTGA	ACCTTCTGGT	360
GCACCTGGCCC	CTGGCTGACT	GCTCTTCTGC	AGGAAGTTGG	AGGAGATTCC	TGAAGTTGAT	420
TCCTCAGGCT	GGATGTCCAA	GGGGGTTGGA	GTTTCTGATG	TCTTTCTGTC	TCCCTCTCTT	480
TTCTTTCTCT	CCCTACCAGG	TCCACTTCTT	TCAGAGGGGC	CTGCGGTGCT	CTAAAAGTTC	540
TCCTGTAAAA	GTTTAGAGCA	AATTGGTTAT	TATTTTAAAA	TCAATAAAAC	TTTTAAAGT	600
ACTAAGACAA	CTTCTAAGAG	GGGAGTGGAC	AGAGGGCCTG	GTGGCAGCTC	ACAGTTTCTT	660
TTCTGACCTT	TGGTCTCACC	CACCAAGTGT	CCCACCTGAG	TGCCCACCTT	GCCCACCTGA	720
GGTAATGCCC	TGGGGCTCCA	CCAGTCCAGA	TCCACAGGGC	GCARCCATGT	GGGAGTGGCG	780
GCTGATTGTT	ACCCAGTAGT	GTTGATAGCA	CATTATTTCAT	AACAGCCAAA	GAGAGGAAGC	840
AACCCAAATG	TCCATTAGCT	GATAAATGGA	TAAATGAAAT	ATGGTACGTC	CGAAGAATGG	900
AATATCATTC	ACCCATGAAA	AAGAACGAAG	TCCAGCACCA	AAACGTGCTA	CAACATGGAT	960
GAACTTCGAT	GACTTTGTGC	CACATGAAAG	AAGAAGCCAG	CCACAAAAGG	CCATATATTG	1020

TATGAAATGA	A	ATG	TCC	AGA	ATG	GGC	AAA	CCC	ATA	GAG	ACA	CAA	AAA	TCT	1070	
		Met	Ser	Arg	Met	Gly	Lys	Pro	Ile	Glu	Thr	Gln	Lys	Ser		
		1				5					10					
CCG	CCA	CCT	CCC	TAC	TCT	CGG	CTG	TCT	CCT	CGC	GAC	GAG	TAC	AAG	CCA	1118
Pro	Pro	Pro	Pro	Tyr	Ser	Arg	Leu	Ser	Pro	Arg	Asp	Glu	Tyr	Lys	Pro	
	15					20					25					
CTG	GAT	CTG	TCC	GAT	TCC	ACA	TTG	TCT	TAC	ACT	GAA	ACG	GAG	GCT	ACC	1166
Leu	Asp	Leu	Ser	Asp	Ser	Thr	Leu	Ser	Tyr	Thr	Glu	Thr	Glu	Ala	Thr	
30					35					40					45	
AAC	TCC	CTC	ATC	ACT	GCT	CCG	GGT	GAA	TTC	TCA	GAC	GCC	AGC	ATG	TCT	1214
Asn	Ser	Leu	Ile	Thr	Ala	Pro	Gly	Glu	Phe	Ser	Asp	Ala	Ser	Met	Ser	
				50					55					60		
CCG	GAC	GCC	ACC	AAG	CCG	AGC	CAC	TGG	TGC	AGC	GTG	GCG	TAC	TGG	GAG	1262
Pro	Asp	Ala	Thr	Lys	Pro	Ser	His	Trp	Cys	Ser	Val	Ala	Tyr	Trp	Glu	
			65					70					75			
CAC	CGG	ACG	CGC	GTG	GGC	CGC	CTC	TAT	GCG	GTG	TAC	GAC	CAG	GCC	GTC	1310
His	Arg	Thr	Arg	Val	Gly	Arg	Leu	Tyr	Ala	Val	Tyr	Asp	Gln	Ala	Val	
		80					85					90				
AGC	ATC	TTC	TAC	GAC	CTA	CCT	CAG	GGC	AGC	GGC	TTC	TGC	CTG	GGC	CAG	1358
Ser	Ile	Phe	Tyr	Asp	Leu	Pro	Gln	Gly	Ser	Gly	Phe	Cys	Leu	Gly	Gln	
	95					100					105					
CTC	AAC	CTG	GAG	CAG	CGC	AGC	GAG	TCG	GTG	CGG	CGA	ACG	CGC	AGC	AAG	1406
Leu	Asn	Leu	Glu	Gln	Arg	Ser	Glu	Ser	Val	Arg	Arg	Thr	Arg	Ser	Lys	
110					115					120					125	
ATC	GGC	TTC	GGC	ATC	CTG	CTC	AGC	AAG	GAG	CCC	GAC	GGC	GTG	TGG	GCC	1454
Ile	Gly	Phe	Gly	Ile	Leu	Leu	Ser	Lys	Glu	Pro	Asp	Gly	Val	Trp	Ala	
				130					135					140		
TAC	AAC	CGC	GGC	GAG	CAC	CCC	ATC	TTC	GTC	AAC	TCC	CCG	ACG	CTG	GAC	1502
Tyr	Asn	Arg	Gly	Glu	His	Pro	Ile	Phe	Val	Asn	Ser	Pro	Thr	Leu	Asp	
			145					150					155			
GCG	CCC	GGC	GGC	CGC	GCC	CTG	GTC	GTG	CGC	AAG	GTG	CCC	CCC	GGC	TAC	1550
Ala	Pro	Gly	Gly	Arg	Ala	Leu	Val	Val	Arg	Lys	Val	Pro	Pro	Gly	Tyr	
		160				165						170				
TCC	ATC	AAG	GTG	TTC	GAC	TTC	GAG	CGC	TCG	GGC	CTG	CAG	CAC	GCG	CCC	1598
Ser	Ile	Lys	Val	Phe	Asp	Phe	Glu	Arg	Ser	Gly	Leu	Gln	His	Ala	Pro	
	175					180					185					
GAG	CCC	GAC	GCC	GCC	GAC	GGC	CCC	TAC	GAC	CCC	AAC	AGC	GTC	CGC	ATC	1646
Glu	Pro	Asp	Ala	Ala	Asp	Gly	Pro	Tyr	Asp	Pro	Asn	Ser	Val	Arg	Ile	
190					195					200					205	
AGC	TTC	GCC	AAG	GGC	TGG	GGG	CCC	TGC	TAC	TCC	CGG	CAG	TTC	ATC	ACC	1694
Ser	Phe	Ala	Lys	Gly	Trp	Gly	Pro	Cys	Tyr	Ser	Arg	Gln	Phe	Ile	Thr	
				210					215					220		
TCC	TGC	CCC	TGC	TGG	CTG	GAG	ATC	CTC	CTC	AAC	AAC	CCC	AGA	TAGTGGCGG	1745	
Ser	Cys	Pro	Cys	Trp	Leu	Glu	Ile	Leu	Leu	Asn	Asn	Pro	Arg			
			225					230					235			
CCCCGGCGGG	AGGGGCGGGT	GGGAGGCCGC	GGCCACCGCC	ACCTGCCGGC	CTCGAGAGGG	1805										
GCCGATGCCC	AGAGACACAG	CCCCCACGGA	CAAAACCCCC	CAGATATCAT	CTACCTAGAT	1865										
TTAATATAAA	GTTTTATATA	TTATATGGAA	ATATATATTA	TACTTGTAAT	TATGGAGTCA	1925										
TTTTTACAAT	GTAATTATTT	ATGTATGGTG	CAATGTGTGT	ATATGGACAA	AACAAGAAAG	1985										
ACGCACTTTG	GCTTATAATT	CTTTCAATAC	AGATATATTT	TCTTTCTCTT	CCTCCTTCCT	2045										
CTTCCTTACT	TTTTATATAT	ATATATAAAG	AAAATGATAC	AGCAGAGCTA	GGTGGAAAAG	2105										
CCTGGGTTTG	GTGTATGGTT	TTTGAGATAT	TAATGCCCAG	ACAAAAAGCT	AATACCAGTC	2165										

ACTCGATAAT	AAAGTATTCG	CATTATAGTT	TTTTTTAAAC	TGTCTTCTTT	TTACAAAGAG	2225
GGGCAGGTAG	GGCTTCAGCG	GATTTCTGAC	CCATCATGTA	CCTTGAAACT	TGACCTCAGT	2285
TTTCAAGTTT	TACTTTTATT	GGATAAAGAC	AGAACAAATT	GAAAAGGGAG	GAAAGTCACA	2345
TTTACTCTTA	AGTAAACCAG	AGAAAGTTCT	GTTGTTCCCT	CCTGCCCCATG	GCTATGGGGT	2405
GTCCAGTGGA	TAGGGATGGC	GGTGGGGAAA	AGGAGAATAC	ACTGGCCATT	TATCCTGGAC	2465
AAGCTCTTCC	AGTCTGATGG	AGGAGGTTCA	TGCCCTAGCC	TAGAAAGGCC	CAGGTCCATG	2525
ACCCCATCT	TTGAGTTATG	AGCAAGCTAA	AAGAAGACAC	TATTTCTCAC	CATTTTGTGG	2585
AAATGGCCTG	GGGAACAAAG	ACTGAAATGG	GCCTTGAGCC	CACCTGCTAC	CTTGCAGAGA	2645
ACCATCTCGA	GCCCCGTAGA	TCTTTTTTAGG	ACCTCCACAG	GSTATTTCCC	ACCCCCCAGC	2705
CAAAAATAGC	TCAGAATCTG	CCCATCCAGG	GCTTGATTA	ATGATTTATG	TAAAGGCAGA	2765
TGGTTTATTT	CTACTTTGTA	AAAGGGAAAA	GTTGAGGTC	TGGAAGGATA	AATGATTTCG	2825
TCATGAGACA	AAATCAAGGT	TAGAAGTTAC	ATGGAATTGT	AGGACCAGAG	CCATATCATT	2885
AGATCAGCTT	TCTGAAGAAT	ATTCTCCAMA	AAAGAAAGTC	TCCTTGGCCA	GATAACTAAG	2945
AGGAATGTTT	CATTGTATAT	CTTTTTTCTT	GGAGATTTAT	ATTAACATAT	TAAGTGCTCT	3005
GAGAAGTCCT	GTGTATTATC	TCTTGCTGCA	TAATAAATTA	TCCCCAMACT	TAAAAAATAA	3065
AAAAAAAAAA	AAACTCGAG					3084

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Ser	Arg	Met	Gly	Lys	Pro	Ile	Glu	Thr	Gln	Lys	Ser	Pro	Pro	Pro
1				5				10						15	
Pro	Tyr	Ser	Arg	Leu	Ser	Pro	Arg	Asp	Glu	Tyr	Lys	Pro	Leu	Asp	Leu
			20					25					30		
Ser	Asp	Ser	Thr	Leu	Ser	Tyr	Thr	Glu	Thr	Glu	Ala	Thr	Asn	Ser	Leu
		35					40					45			
Ile	Thr	Ala	Pro	Gly	Glu	Phe	Ser	Asp	Ala	Ser	Met	Ser	Pro	Asp	Ala
50						55					60				
Thr	Lys	Pro	Ser	His	Trp	Cys	Ser	Val	Ala	Tyr	Trp	Glu	His	Arg	Thr
65					70					75				80	
Arg	Val	Gly	Arg	Leu	Tyr	Ala	Val	Tyr	Asp	Gln	Ala	Val	Ser	Ile	Phe
			85					90					95		
Tyr	Asp	Leu	Pro	Gln	Gly	Ser	Gly	Phe	Cys	Leu	Gly	Gln	Leu	Asn	Leu
			100					105					110		
Glu	Gln	Arg	Ser	Glu	Ser	Val	Arg	Arg	Thr	Arg	Ser	Lys	Ile	Gly	Phe
		115					120					125			
Gly	Ile	Leu	Leu	Ser	Lys	Glu	Pro	Asp	Gly	Val	Trp	Ala	Tyr	Asn	Arg
		130				135					140				
Gly	Glu	His	Pro	Ile	Phe	Val	Asn	Ser	Pro	Thr	Leu	Asp	Ala	Pro	Gly
145					150					155				160	
Gly	Arg	Ala	Leu	Val	Arg	Lys	Val	Pro	Pro	Gly	Tyr	Ser	Ile	Lys	
			165					170					175		
Val	Phe	Asp	Phe	Glu	Arg	Ser	Gly	Leu	Gln	His	Ala	Pro	Glu	Pro	Asp
		180						185					190		
Ala	Ala	Asp	Gly	Pro	Tyr	Asp	Pro	Asn	Ser	Val	Arg	Ile	Ser	Phe	Ala
		195					200					205			
Lys	Gly	Trp	Gly	Pro	Cys	Tyr	Ser	Arg	Gln	Phe	Ile	Thr	Ser	Cys	Pro
	210					215					220				
Cys	Trp	Leu	Glu	Ile	Leu	Leu	Asn	Asn	Pro	Arg					
225					230					235					

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTTTTTTTT TNC 13

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGAGGCGTC 10

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

TGGACCGGTG 10

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

TTTTTTTTTT TNA 13

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 10 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AGACGTCCAC 10

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ACTTCGCCAC 10

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TCGGACGTGA 10

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

CATTTCAATT CATACAA 17

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

CATTTCAATT CATACAATAT ATG 23

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CATTTCAATT CATACAATAT ATGGCCTTT 29

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CATTTTCATT CATACAATAT ATGGCCTTTT GTGGC 35

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGACATTTC TTTCATACAA TATATGGCCT TTTGT 35

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

TTCATTTTCAT ACAATATATG GCCTTTTGT 29

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TCATACAATA TATGGCCTTT TGT 23

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

AATATATGGC CTTTGT

17

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CATGCGGGGC GAGGAGG

17

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CATGCGGGGC GAGGAGGCCA GGA

23

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CATGCGGGGC GAGGAGGCCA GGAGAAAAG

29

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

CATGCGGGGC GAGGAGGCCA GGAGAAAAGT CGTTT

35

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:
GAACATGCGG GGCGAGGAGG CGAGGAGAAA AGTCG 35

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:
GCGGGGCGAG GAGGCGAGGA GAAAAGTCG 29

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 23 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:
CGAGGAGGCG AGGAGAAAAG TCG 23

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:
GGCGAGGAGA AAAGTCG 17

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 24 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:
CAAAGCNGNN NNNNCNGAGN AGUC 24

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 73 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GGUGGAGCCC CAGGGCAUUA CCUCAAAGCN GNNNNNNCNG AGNAGUCGUG GGCAAGGUGG 60
GCACUCAGGU GGG 73

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

GUGUCUCUAU GGGUUUGCCC AAAGCNGNNN NNNCNGAGNA GUCUCUGGAC AUUUCAUUUC 60
AUAC 64

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GGCCCUCUCG CCGUCGGGCU CCUUGCUGAG CAAAGCNGNN NNNNCNGAGN AGUCGAUGCC 60
GAAGCCGAUC UUGCUGCGCG 80

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CGUUUGCCUG CUAAGGAGCG AACAAAGCNG NNNNNNCNGA GNAGUCGAUG UUUCUUUGUG 60
AGUCGGGCGC CG 72

(2) INFORMATION FOR SEQ ID NO:41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

CGCCGGACGA GCGCAGAUCC UUUGGUCCUG AACAAAGCNG NNNNNNCNGA GNAGUCCGGG 60
GCGAGGAGGC GAGGAGAAAA GUCG 84

(2) INFORMATION FOR SEQ ID NO:42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 88 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Other

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GGAGUAAGGA GGGGGGGGAG ACUCUAGUUC GCAAAGCNGN NNNNNCNGAG NAGUCAGUCG
GCUAAGGUGA UGGGGGUUGC AGCACACC

60
88

(2) INFORMATION FOR SEQ ID NO:43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Tyr Thr Asp Thr Gly Lys Ala Ser Gly Asn Leu Glu Thr Lys Tyr Lys
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: unknown
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Thr Gly Lys Lys Ser Gly Lys Leu Lys Ala Ser Tyr Lys Arg Asp
1 5 10 15